

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 14, 2003, 05:30:50 ; Search time 1.75281 Seconds
(without alignments)

1057.973 Million cell updates/sec

Title: US-09-698-781-17

Perfect score: 44

Sequence: 1 TLEPVLFL 9

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

SPREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	203	4	Q9H108
2	39	88.6	421	2	Q9FOX9
3	37	84.1	604	8	Q8W9G3
4	36	81.8	85	2	O85399
5	36	81.8	161	16	Q9KNN5
6	36	81.8	227	8	Q9TBK7
7	36	81.8	408	3	Q9A639
8	35	79.5	222	16	Q9X0H3
9	35	79.5	227	8	Q9B6Y8
10	35	79.5	316	17	Q8TRD3
11	35	79.5	361	16	Q9WYL9
12	35	79.5	501	16	Q98EG2
13	35	79.5	543	16	Q99WT7
14	35	79.5	543	16	Q932E9
15	35	79.5	622	13	O57661
16	35	79.5	826	2	O8RPN1

17	35	79.5	1325	10	Q64533
18	34	77.3	174	16	Q67603
19	34	77.3	177	11	Q9CWD1
20	34	77.3	227	8	Q9X1I9
21	34	77.3	237	16	Q9K8B8
22	34	77.3	246	11	Q9D3K3
23	34	77.3	247	4	Q9H953
24	34	77.3	247	11	Q9DAV4
25	34	77.3	247	11	Q9CR67
26	34	77.3	326	2	Q93OC8
27	34	77.3	330	5	Q9TXH3
28	34	77.3	341	8	Q95B44
29	34	77.3	356	16	Q97J84
30	34	77.3	369	16	Q8RD02
31	34	77.3	373	16	Q8RAJ8
32	34	77.3	405	16	Q995Z8
33	34	77.3	405	16	Q931N2
34	34	77.3	455	2	Q9X479
35	34	77.3	471	2	Q93MR9
36	34	77.3	511	16	Q8YVJ9
37	34	77.3	653	16	Q9HTG5
38	34	77.3	1118	5	Q9N824
39	33	75.0	89	16	Q9CR15
40	33	75.0	101	4	Q9UPH8
41	33	75.0	119	16	Q8XXQ1
42	33	75.0	186	16	Q8XYL2
43	33	75.0	250	4	Q8WU77
44	33	75.0	251	4	Q75549
45	33	75.0	290	16	Q9CMA0

ALIGNMENTS

RESULT 1

Q9H108 PRELIMINARY: PRT: 203 AA.

AC Q9H108:

DT 01-MAR-2001 (TRENBLREL. 16, Created)

DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)

DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)

DE D417L20.1 (Cysteine-rich secretory protein 3 (Crisp-3, SGP28))

DE (Fragment):

GN D417L20.1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Phillimore B.;

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL121974; CAC19654.1;..

DR HSSP: P04284; ICPE.

DR InterPro: IPR001283; Allrgn_V5/TpX1.

DR Pfam: PF00188; SCP. 1.

DR PRINTS: PR00837; V5TPX1KE.

DR ProDom: PD000542; Allrgn_V5/TpX1. 1.

DR SMART: SM00198; SCP. 1.

DR PROSITE: PS01009; SCP_AGS_P1_SC7_1; 1.

DR PROSITE: PS01010; SCP_AGS_P1_SC7_2; 1.

FT NON-TER 203

FT SEQUENCE 203 AA: 22912 MW: F80D707EED081A2B CRC64:

Query Match 100.0%; Score 44; DB 4; Length 203;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TLEPVLFL 9

DB 2 TLEPVLFL 10

RESULT 2

09FOX9 PRELIMINARY; PRT; 421 AA.
 AC 09FOX9;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Putative nitrate/nitrite transporter.
 GN NAD.
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C7R12;
 RX MEDLINE=21240335; PubMed=11342223;
 RA Philpott L., Mirlean P., Mazurker S., Sibiolt S., Hartmann A.,
 Lemanceau P., Geron J.C.;
 RT "Characterization and transcriptional analysis of Pseudomonas
 fluorescens denitrifying clusters containing the nar, nir, nor and nos
 genes.";
 RT Blochim. Biophys. Acta 1517:436-440(2001).
 RL EMBL: AF197465; AAC34371.1;
 DR SEQUENCE 421 AA; 46035 MW; 4D8482587EBA1861 CRC64;
 SQ

Query Match 88.6%; Score 39; DB 2; Length 421;
 Best Local Similarity 77.8%; Pred. No. 21;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLFPVLLFL 9
 Db 314 TLFPVLLFLV 322

RESULT 3

08W9G3 PRELIMINARY; PRT; 604 AA.
 ID 08W9G3;
 AC 08W9G3;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE NADH dehydrogenase subunit 5.
 GN NADH5.
 OS Tachygylossus aculeatus (Australian echidna).
 CC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Monotremata; Tachygylossidae; Tachygylossus.
 OX NCBI_TaxID=9261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=21592585; PubMed=11734900;
 RA Jenke A., Magnelli O., Wiecek G., Westerman M., Arnason U.;
 RT "Phylogenetic analysis of 18S rRNA and the mitochondrial genomes of
 the wombat, Vombat ursinus, and the spiny anteater, Tachygylossus
 aculeatus: Increased support for the Marsupionta Hypothesis.";
 RT J. Mol. Evol. 54:71-80(2002).
 RL EMBL: AJ303116; CAC88020.1;
 DR InterPro: IPR003916; NADhub-oxred5.
 DR InterPro: IPR001750; Oxidored_q1.
 DR InterPro: IPR001516; Oxidored_q1_N.
 DR Pfam: PF00361; Oxidored_q1; 1.
 DR Pfam: PF00662; Oxidored_q1_N; 1.
 DR PRINTS: PRO1434; NADHDGNASES.
 KM Mitochondrion.
 SQ SEQUENCE 604 AA; 67629 MW; 9624D7B3A3F54486 CRC64;

Query Match 84.1%; Score 37; DB 8; Length 604;
 Best Local Similarity 77.8%; Pred. No. 65;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLFPVLLFL 9

Db 48 SLFPVLLFL 56

RESULT 4

085399 PRELIMINARY; PRT; 85 AA.
 ID 085399;
 AC 085399;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Hypothetical 10.1 kDa protein.
 GN Coxiella burnetii.
 OS Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
 CC Coxiella group; Coxiella.
 OX NCBI_TaxID=777;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NINE MILE PHASE I;
 RX MEDLINE=98348442; PubMed=9683477;
 RA Williams H., Jaeger C., Baljer G.;
 RT "Physical and genetic map of the obligate intracellular bacterium
 Coxiella burnetii.";
 RT J. Bacteriol. 180:3816-3822(1998).
 RL EMBL: AF064956; AAD09940.1;
 DR Hypothetical protein.
 KM
 SQ SEQUENCE 85 AA; 10146 MW; 8F67FC9780CD1E2A CRC64;

Query Match 81.8%; Score 36; DB 2; Length 85;
 Best Local Similarity 77.8%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 TLFPVLLFL 9
 Db 25 TAPVLLFL 33

RESULT 5

09KNN5 PRELIMINARY; PRT; 161 AA.
 ID 09KNN5;
 AC 09KNN5;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Fxsa protein.
 GN VC2696.
 OS Vibrio cholerae.
 CC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 Gill S.R., Nelson K.E., Read T.D., Teitelin H., Richardson D.,
 Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dracot I., Sellers P.,
 McDonald L., Uitterlinden T., Fleischmann R.D., Nierman W.C., White O.,
 Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae.";
 RT Nature 406:477-483(2000).
 RL EMBL: AE004335; AAF95837.1;
 DR TIGR: VC2696;
 KM Complete proteome.
 SQ SEQUENCE 161 AA; 17485 MW; 04BD915C81FBE822 CRC64;

Query Match 81.8%; Score 36; DB 16; Length 161;
 Best Local Similarity 75.0%; Pred. No. 33;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LFPVLLFL 9

Db
1 MFPIIFL 8

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RESULT 6
Q9TBK7 PRELIMINARY; PRT; 227 AA.
AC Q9TBK7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE ATP synthase A chain (EC 3.6.1.34).
OS Guirra guirra (Guirra cuckoo).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Cuculiformes; Crotophagidae; Guirra.
OX NCBI_TaxID=30392;
RN [1]
RP MEDLINE=99416451; PubMed=10486983;
RX Hughes J.M., Baker A.J.;
RT "Phylogenetic relationships of the enigmatic hoatzin (Opisthocomus
RT hoatzin) resolved using mitochondrial and nuclear gene sequences."
RL Mol. Biol. Evol. 16:1300-1307(1999).
CC -1- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL. IT MAY PLAY A
CC DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE
CC (BY SIMILARITY).
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
DR EMBL: AF168018; AAD56446.1; -.
DR HSSP: P00855; 1C17.
DR InterPro: IPR000568; ATPsynth_Asub.
DR Pfam: PF00119; ATP-synt_A. 1.
DR PRINTS: PR00123; ATPASEA.
DR TIGRfams: TIGR01131; ATP-synt_6_or_A. 1.
DR PROSITE: PS00449; ATPASE_A. 1.
DR C(0): Hydrogen ion transport; Mitochondrion; Transmembrane.
SQ SEQUENCE 227 AA; 25096 MW; 49472AE8A92F0195 CRC64;

Query Match 81.8%; Score 36; DB 8; Length 227;
Best Local Similarity 87.5%; Pred. NO. 44;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TLFPVLLF 8
Db 24 TLFPALLF 31

RESULT 7
O94639 PRELIMINARY; PRT; 408 AA.
AC O94639;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Putative transporter Cl6D10.06.
GN SPIC16D10.06.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Rajandream M.A., Barrell B.G., Brown D., Churcher C.M.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: TO YEAST ZRT1.

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DR EMBL: AL035637; CAB38510.1; -.
DR InterPro: IPR004698; ZIP_transport.
DR InterPro: IPR003689; zn_trnprt_2ip.
DR Pfam: PF02535; Zip; 1.
DR TIGRfams: TIGR00820; zip; 1.
DR Hypothetical protein; Transmembrane; Transport.
KW TRANSMEM 64
FT TRANSMEM 141 161 POTENTIAL.
FT TRANSMEM 279 299 POTENTIAL.
FT TRANSMEM 315 335 POTENTIAL.
SQ SEQUENCE 408 AA; 45272 MW; 0EB0CAF53CC3F0CE CRC64;

Query Match 81.8%; Score 36; DB 3; Length 408;
Best Local Similarity 75.0%; Pred. NO. 72;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLFPVLLF 8
Db 281 TLFPVILF 288

RESULT 8
Q9X0H3 PRELIMINARY; PRT; 222 AA.
ID Q9X0H3;
AC Q9X0H3;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical protein TM1087.
GN TM1087.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB / DSM 3109.
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RA "Evidence for lateral gene transfer between Archaea and Bacteria from
RA genome sequence of Thermotoga maritima."
RT Nature 398:323-329(1999).
RL Nature 398:323-329(1999).
DR EMBL: AE001768; AAD36164.1; -.
DR TIGR: TM1087; -.
DR InterPro: IPR002610; Rhomboid.
DR Pfam: PF01694; Rhomboid; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 222 AA; 25929 MW; 727793AEC176E50 CRC64;

Query Match 79.5%; Score 35; DB 16; Length 222;
Best Local Similarity 66.7%; Pred. NO. 66;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 TLFPVLLF 9
Db 156 TLFPVILF 164

RESULT 9
O9B6Y8 PRELIMINARY; PRT; 227 AA.
ID O9B6Y8;
AC O9B6Y8;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE ATP synthase A chain (EC 3.6.1.34).
OS Casuarina bennettii (Dwarf cassowary), and
OS Casuarina casuarina (Australian cassowary) (Double-wattled cassowary).
OG Mitochondrion.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauaria; Aves; Palaeognathae; Casuariformes; Casuariidae;
 OC Casuarii.
 OX NCBI_TaxID=30463, 8787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=C.bennetti; TISSUE=MUSCLE;
 RX MEDLINE=21085666; PubMed=11217857;
 RA Cooper A., Lalueza-Fox C., Anderson S., Rambaut A., Austin J.,
 Ward R.;
 RT "Complete mitochondrial genome sequences of two extinct moas clarify
 RT rattle evolution";
 RL Nature 409:704-707(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=C.casuaris;
 RX MEDLINE=21263106; PubMed=11370967;
 RA Haddath O., Baker A.J.;
 RT "Complete mitochondrial DNA genome sequences of extinct birds: rattle
 RT phylogenetics and the vicariance biogeography hypothesis";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 268:939-945(2001).
 CC -1- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL. IT MAY PLAY A
 CC DIRECT ROLE IN THE TRANSLLOCATION OF PROTONS ACROSS THE MEMBRANE
 CC (BY SIMILARITY).
 CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
 CC HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 DR EMBL: AY016011; AK098558.1; -
 DR EMBL: AF338713; AK53319.1; -
 DR InterPro: IPR000368; ATPase_n_Asub.
 DR Pfam: PF00119; ATP_syn_A.1.
 DR PRINTS: PR00123; ATPASEA.
 DR TIGR: TIGR01131; ATP_syn_6_or_A.1.
 DR PROSITE: PS00449; ATPASE_A.1.
 KW CF(0); Hydrogen ion transport; Mitochondrion; Transmembrane.
 SO SEQUENCE 227 AA; 24981 MW; 9A5ADBD8D08BF6C3 CRC64;

Query Match 79.5%; Score 35; DB 8; Length 227;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LFPVLLF 8
 DB 25 LFPVLLF 31

RESULT 10
 O8TRD3 PRELIMINARY; PRT; 316 AA.
 AC O8TRD3;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Oligopeptide ABC transporter, permease.
 GN OPPB OR MA1247.
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;
 RX MEDLINE=21929760; PubMed=11932238;
 RA Galagan J.E., Nussbaum C., Roy A., Endrizzi M.G., Macdonald P.,
 Fitzhugh W., Calvo S., Engels R., Smirnov S., Ancoor D., Brown A.,
 Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
 Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
 Zimmer A., Barber R.D., Cann I., Graham D.E., Graham D.A., Guss A.M.,
 Hedderlich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
 Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
 RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
 RA Metcalf W.W., Birren B.;
 RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
 RT and physiological diversity";
 RL Genome Res. 12:532-542(2002).
 DR EMBL: AE010792; AAM04666.1; -
 KW Complete proteome.
 SO SEQUENCE 316 AA; 35015 MW; 3FA23DB0D54F70D9 CRC64;

Query Match 79.5%; Score 35; DB 17; Length 316;
 Best Local Similarity 75.0%; Pred. No. 89;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LFPVLLF 9
 DB 13 LFPVLLF 20

RESULT 11
 O9WYL9 PRELIMINARY; PRT; 361 AA.
 AC O9WYL9;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein TM0388.
 GN TM0388.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB / DSM 3109;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Liner K.D., Garrett M.W.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequence of Thermotoga maritima";
 RL Nature 399:323-329(1999).
 DR EMBL: AE001718; AAD35473.1; -
 DR TIGR: TM0388; -
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 361 AA; 41105 MW; 72967E8C49D323DA CRC64;

Query Match 79.5%; Score 35; DB 16; Length 361;
 Best Local Similarity 75.0%; Pred. No. 99;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LFPVLLF 9
 DB 25 LFPVLLF 32

RESULT 12
 O98EG2 PRELIMINARY; PRT; 501 AA.
 AC O98EG2;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein ml14258.
 GN ML14258.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-MAFF303099;
 RX MEDLINE-21082930; PubMed-11214968;
 RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 Takeuchi C., Yamada M., Tabata S.;
 RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti."
 RT DNA Res. 7:331-338(2000).
 DR EMBL: AP003003; BAB50957.1;
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 501 AA; 54314 MW; E70D4239DC3A929 CRC64;

Query Match 79.5%; Score 35; DB 16; Length 501;
 Best Local Similarity 77.8%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LFPVLLFL 9
 DB 28 LFPVLLFL 36

RESULT 13

099VT7 PRELIMINARY: PRT; 543 AA.

DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical protein SA0639.

GN SA0639.
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-21311952; PubMed-11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 Cui L., Oguchi A., Aoki K.I., Nagai Y., Iino T., Kanamori M.,
 Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
 Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
 Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
 Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
 Ogasawara N., Hayashi H., Hiramatsu K.;
 RA "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus."
 RT Lancet 357:1225-1240(2001).
 DR EMBL: AP003131; BAB41872.1;
 DR HSSP: P13569; INBD.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR001140; ABCtransportrTM.
 DR InterPro: IPR003439; ABC_transportr.
 DR Pfam: PF00664; ABC_membrane; 1.
 DR Pfam: PF00005; ABC_tran; 1.
 DR ProDom: PD000006; ABC_transportr; 1.
 DR SMART: SM00382; AAA; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 DR KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 543 AA; 61908 MW; F74F7863EF64B21 CRC64;

Query Match 79.5%; Score 35; DB 16; Length 543;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LFPVLLFL 9
 DB 13 LFPVLLFL 20

RESULT 14

0932E9 PRELIMINARY: PRT; 543 AA.

AC 0932E9;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical protein SAV0684.

GN SAV0684.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-21311952; PubMed-11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 Cui L., Oguchi A., Aoki K.I., Nagai Y., Iino T., Kanamori M.,
 Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.I., Kaito C.,
 Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RA "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus."
 RT Lancet 357:1225-1240(2001).
 DR EMBL: AP003130; BAB56846.1;
 DR InterPro: IPR001140; ABCtransportrTM.
 DR InterPro: IPR003439; ABC_transportr.
 DR Pfam: PF00664; ABC_membrane; 1.
 DR Pfam: PF00005; ABC_tran; 1.
 DR ProDom: PD000006; ABC_transportr; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 DR KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 543 AA; 61909 MW; 754E8CBF3458A25 CRC64;

Query Match 79.5%; Score 35; DB 16; Length 543;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LFPVLLFL 9
 DB 13 LFPVLLFL 20

057661 PRELIMINARY: PRT; 622 AA.

DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Intestinal sodium/lithium-dependent dicarboxylate transporter
 DE (NA(+)/dicarboxylate cotransporter).
 GN NADC-2.

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8335;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE;
 RX MEDLINE-97423461; PubMed-9277403;

RA Bai L., Pajor A.M.;
 RT Expression cloning of NADC-2, an intestinal Na(+)- or Li(+)-dependent
 RT dicarboxylate transporter.
 RL Am. J. Physiol. 273:G267-G274(1997).
 CC -1- FUNCTION: TRANSPORTS DI- AND TRICARBOXYLATES, INCLUDING SUCCINATE,
 CC CITRATE, AND GLUTARATE, BUT EXCLUDES THE MONOCARBOXYLATE LACTATE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC DR EMBL: U07318; AAB97879.1;
 DR InterPro: IPR001898; Na/sulf_symp.

DR Pfam: PF00939; Na_sulph_symp: 1.
DR PROSITE: PS01271; NA_SULFATE; FALSE_NEG.
KM Transport; Transmembrane; Sodium transport; Symport.
FT TRANSMEM 13 33 POTENTIAL.
FT TRANSMEM 53 73 POTENTIAL.
FT TRANSMEM 114 134 POTENTIAL.
FT TRANSMEM 259 279 POTENTIAL.
FT TRANSMEM 299 319 POTENTIAL.
FT TRANSMEM 366 386 POTENTIAL.
FT TRANSMEM 411 431 POTENTIAL.
FT TRANSMEM 456 476 POTENTIAL.
FT TRANSMEM 494 514 POTENTIAL.
FT TRANSMEM 542 562 POTENTIAL.
FT TRANSMEM 584 604 POTENTIAL.
FT DOMAIN 123 126 POLY-LEU.
FT CARBOHYD 617 617 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 622 AA; 68550 MW; D25C06BB806B0098 CRC64;

Query Match 79.5%; Score 35; DB 13; Length 622;

Best Local Similarity 100.0%; Pred. NO. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LFPVTLF 8

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Db 61 LFPVTLF 67

Search completed: March 14, 2003, 05:43:02
Job time : 4.75281 secs